\_\_\_\_\_\_

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)

217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Wed Aug 08 14:07:27 EDT 2007

\_\_\_\_\_\_

\*\*\*\*\*\*\*\*\*\*\*\*\*

Reviewer Comments:

<160> 13

Although the above <160> response is "13," 18 sequences are shown in the submitted file. See below:

<210> 18

<211> 225

<212> PRT

<213> Mus musculus

<400> 18

Met Leu Leu Thr Leu Ala Gly Gly Ala Leu Phe Phe Pro Gly Leu Phe

(the above is a sample of Sequence 18, the last sequence in the file)

## Validated By CRFValidator v 1.0.2

Application No: 10536772 Version No: 2.0

Input Set:

Output Set:

**Started:** 2007-08-06 11:18:39.445

**Finished:** 2007-08-06 11:18:41.545

**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 100 ms

Total Warnings: 11

Total Errors: 13

No. of SeqIDs Defined: 13

Actual SeqID Count: 18

Error code		Error Description
Ε	201	Mandatory field data missing in <223> in SEQ ID (1)
W	213	Artificial or Unknown found in <213> in SEQ ID (3)
E	224	$<\!220\!>\!,<\!223\!>$ section required as $<\!213\!>$ has Artificial sequence or Unknown in SEQID (3)
W	213	Artificial or Unknown found in <213> in SEQ ID (4)
E	224	$<\!220\!>\!,<\!223\!>$ section required as $<\!213\!>$ has Artificial sequence or Unknown in SEQID (4)
W	213	Artificial or Unknown found in <213> in SEQ ID (5)
E	224	$<\!220\!>\!,<\!223\!>$ section required as $<\!213\!>$ has Artificial sequence or Unknown in SEQID (5)
W	213	Artificial or Unknown found in <213> in SEQ ID (6)
E	224	<220>, $<223>$ section required as $<213>$ has Artificial sequence or Unknown in SEQID (6)
W	213	Artificial or Unknown found in <213> in SEQ ID (7)
E	224	$<\!220\!>\!,<\!223\!>$ section required as $<\!213\!>$ has Artificial sequence or Unknown in SEQID (7)
W	213	Artificial or Unknown found in <213> in SEQ ID (8)
E	224	$<\!220\!>\!,<\!223\!>$ section required as $<\!213\!>$ has Artificial sequence or Unknown in SEQID (8)
W	213	Artificial or Unknown found in <213> in SEQ ID (9)
E	224	$<\!220\!>\!,<\!223\!>$ section required as $<\!213\!>$ has Artificial sequence or Unknown in SEQID (9)
W	213	Artificial or Unknown found in <213> in SEQ ID (10)

## Input Set:

## Output Set:

**Started:** 2007-08-06 11:18:39.445 **Finished:** 2007-08-06 11:18:41.545

**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 100 ms

Total Warnings: 11
Total Errors: 13

No. of SeqIDs Defined: 13

Actual SeqID Count: 18

Error code		Error Description
E	224	$<\!220\!>\!, <\!223\!>$ section required as $<\!213\!>$ has Artificial sequence or Unknown in SEQID (10)
W	213	Artificial or Unknown found in <213> in SEQ ID (11)
E	224	$<\!220\!>, <\!223\!>$ section required as $<\!213\!>$ has Artificial sequence or Unknown in SEQID (11)
W	213	Artificial or Unknown found in <213> in SEQ ID (12)
E	224	$<\!220\!>, <\!223\!>$ section required as $<\!213\!>$ has Artificial sequence or Unknown in SEQID (12)
W	213	Artificial or Unknown found in <213> in SEQ ID (13)
E	224	$<\!220\!>, <\!223\!>$ section required as $<\!213\!>$ has Artificial sequence or Unknown in SEQID (13)
E	252	Calc# of Seq. differs from actual; 13 seqIds defined; count=18

## Sequence listing

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                                                                        114
                                    Met Leu Leu Thr Leu Ala Gly Gly
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   gcg ctc ttc ttc ccg ggg ctc ttc gcg ctc tgc acc tgg gcg ctg cgc
                                                                        162
   Ala Leu Phe Phe Pro Gly Leu Phe Ala Leu Cys Thr Trp Ala Leu Arg
   cac tcc cag ccc gga tgg agc cgc acc gac tgc gtg atg atc agc acc
                                                                        210
   His Ser Gln Pro Gly Trp Ser Arg Thr Asp Cys Val Met Ile Ser Thr
                                           35
                       30
   agg ctg gtt tcc tcg gtg cac gcc gtg ctg gcc acc ggc tcg ggg atc
                                                                        258
   Arg Leu Val Ser Ser Val His Ala Val Leu Ala Thr Gly Ser Gly Ile
   gtc atc att cgc tcc tgc gac gac gtg atc acc ggc agg cac tgg ctt
                                                                        306
   Val Ile Ile Arg Ser Cys Asp Asp Val Ile Thr Gly Arg His Trp Leu
                                   65
   gcc cgg gaa tat gtg tgg ttt ctg att cca tac atg atc tat gac tcg
                                                                        354
   Ala Arg Glu Tyr Val Trp Phe Leu Ile Pro Tyr Met Ile Tyr Asp Ser
           75
                               80
                                                   85
                                                                        402
   tac gcc atg tac ctc tgt gaa tgg tgc cga acc aga gac cag aac cgt
   Tyr Ala Met Tyr Leu Cys Glu Trp Cys Arg Thr Arg Asp Gln Asn Arg
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105					110					115					120	
atc	aca	cat	cat	gcg	gtc	att	ctc	ctt	gtc	ctt	gtg	cca	gtc	gca	cag	498
Ile	Thr	His	His		Val	Ile	Leu	Leu		Leu	Val	Pro	Val		Gln	
				125					130					135		
			gga -	-			-			-		-			-	546
Arg	Leu	Arg	Gly	Asp	Leu	Gly	Asp		Phe	Val	Gly	Cys		Phe	Thr	
			140					145					150			
_	_	_	agc		_			_	_			_	_		_	594
Ala	Glu		Ser	Thr	Pro	Phe		Ser	Leu	Gly	Arg		Leu	Ile	Gln	
		155					160					165				
	_	_	cag				_		_						-	642
Leu	_	Gln	Gln	His	Thr		Leu	Tyr	Lys	Val		Gly	Ile	Leu	Thr	
	170					175					180					
ctg	gcc	acc	ttc	ctt	tcc	tgc	cgg	atc	ctt	ctc	ttc	CCC	ttc	atg	tac	690
Leu	Ala	Thr	Phe	Leu	Ser	Суз	Arg	Ile	Leu	Leu	Phe	Pro	Phe	Met	Tyr	
185					190					195					200	
tgg	tcc	tat	ggc	cgc	cag	cag	gga	cta	agc	ctg	ctc	caa	gta	CCC	ttc	738
Trp	Ser	Tyr	Gly	Arg	Gln	Gln	Gly	Leu	Ser	Leu	Leu	Gln	Val	Pro	Phe	
				205					210					215		
agc	atc	cca	ttc	tac	tgc	aac	gtg	gcc	aat	gcc	ttc	ctc	gta	gct	cct	786
Ser	Ile	Pro	Phe	Tyr	Cys	Asn	Val	Ala	Asn	Ala	Phe	Leu	Val	Ala	Pro	
			220					225					230			
cag	atc	tac	tgg	ttc	tgt	ctg	ctg	tgc	agg	aag	gca	gtc	cgg	ctc	ttt	834
Gln	Ile	Tyr	Trp	Phe	Cys	Leu	Leu	Cys	Arg	Lys	Ala	Val	Arg	Leu	Phe	
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															tactg	1721
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atga	attt	aa q	gacto	gtgct	a co	catgt	gtto	e tea	aagto	ggta	gttt	aaaa	aag t	ggat	tttta	2081
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Val Leu Ala Thr Gly Ser Gly Ile Val Ile Ile Arg Ser Cys Asp Asp
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Val Ile Thr Gly Arg His Trp Leu Ala Arg Glu Tyr Val Trp Phe Leu
                70
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Ile Pro Tyr Met Ile Tyr Asp Ser Tyr Ala Met Tyr Leu Cys Glu Trp
            85 90
Cys Arg Thr Arg Asp Gln Asn Arg Ala Pro Ser Leu Thr Leu Arg Asn
         100 105
Phe Leu Ser Arg Asn Arg Leu Met Ile Thr His His Ala Val Ile Leu
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Leu Val Leu Val Pro Val Ala Gln Arg Leu Arg Gly Asp Leu Gly Asp
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Phe Phe Val Gly Cys Ile Phe Thr Ala Glu Leu Ser Thr Pro Phe Val
145 150
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Ser Leu Gly Arg Val Leu Ile Gln Leu Lys Gln Gln His Thr Leu Leu
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Tyr Lys Val Asn Gly Ile Leu Thr Leu Ala Thr Phe Leu Ser Cys Arg
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Ile Leu Leu Phe Pro Phe Met Tyr Trp Ser Tyr Gly Arg Gln Gln Gly
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Leu Ser Leu Leu Gln Val Pro Phe Ser Ile Pro Phe Tyr Cys Asn Val
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Ala Asn Ala Phe Leu Val Ala Pro Gln Ile Tyr Trp Phe Cys Leu Leu
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Lys His Gln Val Lys Gly His Gly Gly Asp Asp Gly Ala Ala Arg Ala
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Pro Gly Ser Thr Trp Ala Ile Ala Arg Gly Tyr Leu His Lys Glu Phe
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Leu Met Val Leu His His Ala Ala Met Val Leu Val Cys Phe Pro Leu
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Ser Val Val Trp Arg Gln Gly Lys Gly Asp Phe Phe Leu Gly Cys Met
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Leu Met Ala Glu Val Ser Thr Pro Phe Val Cys Leu Gly Lys Ile Leu
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Ile Gln Tyr Lys Gln Gln His Thr Leu Leu His Lys Val Asn Gly Ala
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Leu Met Leu Leu Ser Phe Leu Cys Cys Arg Val Leu Leu Phe Pro Tyr
         150 155 160
Leu Tyr Trp Ala Tyr Gly Arg His Ala Gly Leu Pro Leu Leu Ala Val
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10

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35 40 45

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50 55 60

His Ile Ile Asp Asp Gln His Trp Leu Ser Ser Ala Tyr Thr Gln Phe 65 70 75 80

Ala Val Pro Tyr Phe Ile Tyr Asp Ile Tyr Ala Met Phe Leu Cys His 85 90 95

Trp His Lys His Gln Val Lys Gly His Gly Gly Glu Asp Gly Thr Pro  $100 \hspace{1cm} 105 \hspace{1cm} 110 \hspace{1cm}$ 

Arg Ala Leu Gly Ser Thr Trp Ala Val Val Arg Gly Tyr Leu His Lys 115 120 125

Glu Phe Leu Met Val Leu His His Ala Ala Met Val Leu Val Cys Phe 130 135 140

Cys Met Leu Met Ala Glu Val Ser Thr Pro Phe Val Cys Leu Gly Lys
165 170 175

Ile Leu Ile Gln Tyr Lys Gln Gln His Thr Leu Leu His Lys Val Asn 180 185 190

Gly Ala Leu Met Leu Leu Ser Phe Leu Cys Cys Arg Val Leu Leu Phe 195 200 205

Pro Tyr Leu Tyr Trp Ala Tyr Gly Arg His Ala Gly Leu Pro Leu Leu 210 215 220

Ser Val Pro Met Ala Ile Pro Ala His Val Asn Leu Gly Ala Ala Leu 225 230 235 240

Leu Leu Ala Pro Gln Leu Tyr Trp Phe Phe Leu Ile Cys Arg Gly Ala
245 250 255

Cys Arg Leu Phe Arg Pro Arg Gly Ser Pro Pro Pro Ser Pro Cys Gln 260 265 270

Thr Gln Asp 275

<210> 16

<211> 353

<212> PRT

<213> Homo sapiens

<400> 16

Leu Ala Ile Pro Ser Ser Pro Pro Thr Pro Ser Leu Asn Leu Ala Phe
1 5 10 15

Leu Ser Leu Leu Asp Pro Leu Val Ser Leu Pro Gly Phe Lys Ser Pro 20 25 30

Cys Leu Pro Gln Trp Trp Leu Gly Gly Trp Cys Ser Pro Asp Ser Ser 35 40 45

Ser Tyr Pro Arg Thr Arg Ser Arg Gly Cys Pro Ser Cys Ala Gly Arg 50 55 60

Glu Ala Asp Ala Val Ile Val Ser Ala Arg Leu Val Ser Ser Val Gln 65 70 75 80

Ala Ile Met Ala Ser Thr Ala Gly Tyr Ile Val Ser Thr Ser Cys Lys 85 90 95

His Ile Ile Asp Asp Gln His Trp Leu Ser Ser Ala Tyr Thr Gln Phe 100 105 110

Ala Val Pro Tyr Phe Ile Tyr Asp Ile Tyr Ala Met Phe Leu Cys His

115 120 125

Trp	His	Lys	His	Gln	Val	Lys	Gly	His	Gly	Gly	Glu	Asp	Gly	Thr	Pro
	130					135					140				
Arg	Ala	Leu	Gly	Ser	Thr	Trp	Ala	Val	Val	Arg	Gly	Tyr	Leu	His	Lys
145					150					155					160
Glu	Phe	Leu	Met	Val	Leu	His	His	Ala	Ala	Met	Val	Leu	Val	Cys	Ph∈
				165					170					175	
Pro	Leu	Ser	Val	Val	Trp	Arg	Gln	Gly	Lys	Gly	Asp	Phe	Phe	Leu	Gly
			180					185					190		
Cys	Met	Leu	Met	Ala	Glu	Val	Ser	Thr	Pro	Phe	Val	Cys	Leu	Gly	Lys
		195					200					205			
Ile	Leu	Ile	Gln	Tyr	Lys	Gln	Gln	His	Thr	Leu	Leu	His	Lys	Val	